



#8/C

SUBSTITUTE SEQUENCE LISTING

<110> GVS Gesellschaft Fur Erwerb und Verwertung von Schutzrechten-GVS mbH and
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Heinz, Ernst
Zahringer, Ulrich

<120> Processive Sugar Transferase

<130> MAIWAM2.001CP1

<140> US 09/668,788
<141> 2000-09-22

<150> PCT/DE99/00857
<151> 1999-03-25

<150> DE 198 13 017.1
<151> 1998-03-25

<150> DE 198 19 958.9
<151> 1998-05-05

<160> (4) ✓

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<212> DNA
<213> Bacillus subtilis

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1149

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<211> 382
<212> PRT
<213> Bacillus subtilis

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Gly Phe Gln His Val Thr Val Ser Asn Leu Tyr Gln Glu Ser Asn Pro
35 40 45
Ile Val Ser Glu Val Thr Gln Tyr Leu Tyr Leu Lys Ser Phe Ser Ile
50 55 60
Gly Lys Gln Phe Tyr Arg Leu Phe Tyr Tyr Gly Val Asp Lys Ile Tyr
65 70 75 80
Asn Lys Arg Lys Phe Asn Ile Tyr Phe Lys Met Gly Asn Lys Arg Leu
85 90 95
Gly Glu Leu Val Asp Glu His Gln Pro Asp Ile Ile Ile Asn Thr Phe
100 105 110
Pro Met Ile Val Val Pro Glu Tyr Arg Arg Arg Thr Gly Arg Val Ile
115 120 125
Pro Thr Phe Asn Val Met Thr Asp Phe Cys Leu His Lys Ile Trp Val
130 135 140
His Glu Asn Val Asp Lys Tyr Tyr Val Ala Thr Asp Tyr Val Lys Glu
145 150 155 160
Lys Leu Leu Glu Ile Gly Thr His Pro Ser Asn Val Lys Ile Thr Gly
165 170 175
Ile Pro Ile Arg Pro Gln Phe Glu Glu Ser Met Pro Val Gly Pro Ile
180 185 190
Tyr Lys Tyr Asn Leu Ser Pro Asn Lys Lys Val Leu Leu Ile Met
195 200 205
Ala Gly Ala His Gly Val Leu Lys Asn Val Lys Glu Leu Cys Glu Asn
210 215 220
Leu Val Lys Asp Asp Gln Val Gln Val Val Val Cys Gly Lys Asn
225 230 235 240
Thr Ala Leu Lys Glu Ser Leu Ser Ala Leu Glu Ala Glu Asn Gly Asp
245 250 255
Lys Leu Lys Val Leu Gly Tyr Val Glu Arg Ile Asp Glu Leu Phe Arg
260 265 270
Ile Thr Asp Cys Met Ile Thr Lys Pro Gly Gly Ile Thr Leu Thr Glu
275 280 285
Ala Thr Ala Ile Gly Val Pro Val Ile Leu Tyr Lys Pro Val Pro Gly
290 295 300
Gln Glu Lys Glu Asn Ala Asn Phe Phe Glu Asp Arg Gly Ala Ala Ile
305 310 315 320
Val Val Asn Arg His Glu Glu Ile Leu Glu Ser Val Thr Ser Leu Leu
325 330 335
Ala Asp Glu Asp Thr Leu His Arg Met Lys Lys Asn Ile Lys Asp Leu
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<212> DNA
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attgagcacg atttatttat ggaagctcat ccaattttga cttctatttga taaaaaatgg 180
tatatcaata gctttaaaaata ttttagaaat atgtacaaag ggtttttatta cagccgccc 240
gataaacttag acaaataatgttt ttacaataac tatggactta ataagttat taatttattt 300
ataaaaagaaa agccagattt aatatttata acgtttccta caccagttat gtcggacta 360
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aaaaactgga ttacgcccgtt ttacaacaaga tattatgtgg caacaaaaga aacgaaacaa 480
gacttcatag acgttaggtat tgatccttca acagttaaag tgacaggtat tccttattt 540
aacaatttg aaacgcctat taatcaaaaag cagtggtaa tagacaacaa cttagatcca 600
gataagcaaa ctatTTtaat gtcaagctggc gcattttggc tatctaaagg ttttgacacg 660
atgattactg atatatttagc gaaaagtgc aatgcacaag tagttatgtat ttgtggtaag 720
agcaaagagc taaagcggtt ttaacagct aagtttaaat taacgagaat gtatttgattt 780
ctaggttata ccaaacacat gaatgaatgg atggcatcaa gtcaacttat gattacgaaa 840
cctgggtgtt tcacaataac tgaaggtttgc gcccgttgta ttccaatgtat ttccctaaat 900
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20 25 30
Met Asn Leu Asp His Leu Ser Val Ile Glu His Asp Leu Phe Met Glu
35 40 45
Ala His Pro Ile Leu Thr Ser Ile Cys Lys Lys Trp Tyr Ile Asn Ser
50 55 60
Phe Lys Tyr Phe Arg Asn Met Tyr Lys Gly Phe Tyr Tyr Ser Arg Pro
65 70 75 80
Asp Lys Leu Asp Lys Cys Phe Tyr Lys Tyr Gly Leu Asn Lys Leu
85 90 95
Ile Asn Leu Leu Ile Lys Glu Lys Pro Asp Leu Ile Leu Leu Thr Phe
100 105 110
Pro Thr Pro Val Met Ser Val Leu Thr Glu Gln Phe Asn Ile Asn Ile
115 120 125
Pro Val Ala Thr Val Met Thr Asp Tyr Arg Leu His Lys Asn Trp Ile
130 135 140
Thr Pro Tyr Ser Thr Arg Tyr Tyr Val Ala Thr Lys Glu Thr Lys Gln
145 150 155 160
Asp Phe Ile Asp Val Gly Ile Asp Pro Ser Thr Val Lys Val Thr Gly
165 170 175
Ile Pro Ile Asp Asn Lys Phe Glu Thr Pro Ile Asn Gln Lys Gln Trp
180 185 190
Leu Ile Asp Asn Asn Leu Asp Pro Asp Lys Gln Thr Ile Leu Met Ser
195 200 205

Ala Gly Ala Phe Gly Val Ser Lys Gly Phe Asp Thr Met Ile Thr Asp
210 215 220
Ile Leu Ala Lys Ser Ala Asn Ala Gln Val Val Met Ile Cys Gly Lys
225 230 235 240
Ser Lys Glu Leu Lys Arg Ser Leu Thr Ala Lys Phe Lys Leu Thr Arg
245 250 255
Met Tyr Leu Ile Leu Gly Tyr Thr Lys His Met Asn Glu Trp Met Ala
260 265 270
Ser Ser Gln Leu Met Ile Thr Lys Pro Gly Gly Ile Thr Ile Thr Glu
275 280 285
Gly Phe Ala Arg Cys Ile Pro Met Ile Phe Leu Asn Pro Ala Pro Gly
290 295 300
Gln Glu Leu Glu Asn Ala Phe Tyr Phe Glu Glu Lys Gly Phe Gly Lys
305 310 315 320
Ile Ala Asp Thr Pro Glu Glu Ala Ile Lys Ile Val Ala Ser Leu Thr
325 330 335
Asn Gly Asn Glu Gln Leu Thr Asn Met Ile Ser Thr Met Glu Gln Asp
340 345 350
Lys Ile Lys Tyr Ala Thr Gln Thr Ile Cys Arg Asp Leu Leu Asp Leu
355 360 365
Ile Gly His Ser Ser Gln Pro Gln Glu Ile Tyr Gly Lys Val Pro Leu
370 375 380
Tyr Ala Arg Phe Phe Val Lys
385 390